



Figure S2. Comparison of uFG-NEM and exhaustive NEM model search for structure recovery. Each bar shows the mean and standard deviation of precision or recall for S-gene links over 100 artificial networks with five S-genes. Networks were generated with no inhibition and an average of 20 E-genes per S-gene. Expression was generated for one replicate using standard deviation of 1 and a mean for the down distribution of -1.75. Precision and recall for both uFG-NEM and exhaustive NEM search do not differ significantly.